GROUP SELECTION EDGE EFFECTS ON THE VASCULAR PLANT COMMUNITY OF A SIERRA NEVADA OLD-GROWTH FOREST

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Abstract

For an old-growth forest edge in the Sierra Nevada, we quantified the extent of edge effects from a group selection harvest. Across transects from the interior of the old-growth forest through the group selection opening, we quantified changes in resource availability (light, soil moisture, and seedbed) and vegetation composition (cover, richness). We found a steep change in light availability and community composition from the intact old-growth to the group selection. Both parametric and non-parametric multivariate analyses indicated two distinct plant associations, old-growth and group selection, with little indication of an edge association. Understory plant species richness normalized to a total area sampled of 0.25 ha was significantly greater in the group selection (74 species) than in the old-growth (55 species). *Chimaphila umbellata* and *Carex brainerdii* were the most abundant species in the old-growth and group selection respectively. *Tragopogon dubius* was the most abundant of six exotic species found in the group selection while there were no nonnative species found in the old-growth forest.

Key Words: Edge effects, group selection, plant diversity, Sierra Nevada, Old-growth.

The competing demands for timber products and forest preservation require land managers to evaluate simultaneously production and conservation objectives (Lindenmayer and Franklin 2002). For the Sierra Nevada of California, group selection has been proposed as a silviculture system that may accommodate production and conservation objectives (e.g., Herger-Feinstein 1998; USDA Forest Service 2002; USDA Forest Service 2003), but there is little quantitative information on the efficacy of such a system.

Group selection involves the periodic harvest of small groups of trees, typically between 0.1 and 1 ha (McDonald and Abbot 1994). Over the long term, a shifting mosaic of small patches of trees develops across the landscape. These patches will inevitably create a relatively large fraction of edge environment (e.g., York et al. 2003). In the context of group selection silviculture, the edge refers to the boundary between the opening created by harvesting a group of trees and the matrix of intact forest. York et al. (2003) reported a substantial edge effect on tree growth in group selection harvests. Given the significant influence of edges on ecological processes, other impacts are likely. In this paper, we assess the width and extent of potential edge influences on understory vascular plants at a forest-to-group edge created by a group selection harvest.

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Study Site

We conducted our study in a mixed conifer forest at the Plumas National Forest. Data was collected from a single group selection harvest and an adjacent long-term plot, the Baker plot (39°55′16″N 121°02′21″W). The Baker plot is a 4.5 ha old-growth mixed conifer stand with no record of recent fire (Ansley and Battles 1998).

The 1-ha group was harvested in 1993 at the north end of the Baker Plot. All overstory trees were felled and the remaining slash was piled and burned. Before planting ponderosa pine, the group was broadcast-burned. The area immediately adjacent to the Baker plot (a buffer approximately 12 m wide) was logged but not burned or replanted. To check for similarity in structure between the old-growth and harvested area, we reconstructed stand basal area from stump diameters and taper equations (Wensel and Olson 1995). Our estimates of basal area in the group selection plots fell well within the observed range of variation for plots of this size in the old-growth stand (59–148 m^2 ha^{-1}, Ansley 1998).

Sampling Design

In 2000, we established three parallel transects along the gradient from the intact forest into the group selection (Fig. 1). Each 100-m long transect consisted of six equally spaced circular 0.031 ha plots. We designated plots along the dripline of the forest canopy as edge plots (0 m). The old-growth plots on the transect were then located −40 m, −20 m away from the drip line, while the group selection plots were located +20 m, +40 m and +60 m into the group selection.

Each circular study plot consisted of four 10 m

Baker Plot (USFS special use permit) (4.7 ha)   Group Selection (1ha)
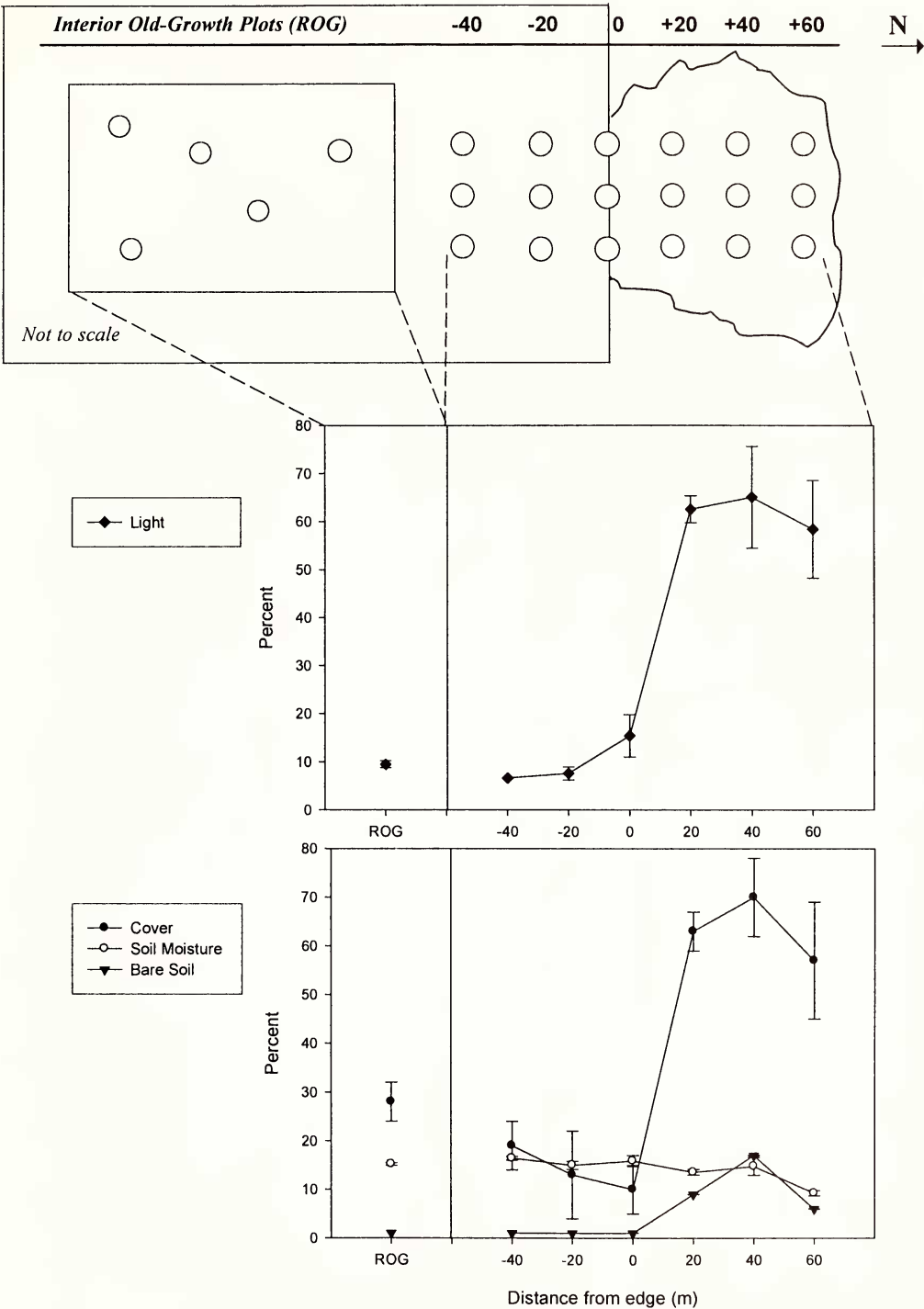
FIG. 1. (Top) Site layout at Baker old-growth forest, Plumas National Forest, California (Bottom) Mean and standard error of light availability at 1-m height (% TTR), understory plant cover measured by percent cover, soil moisture and bare soil for the 3 transects spanning the old-growth forest and group selection as well as the random old-growth plots (ROG).
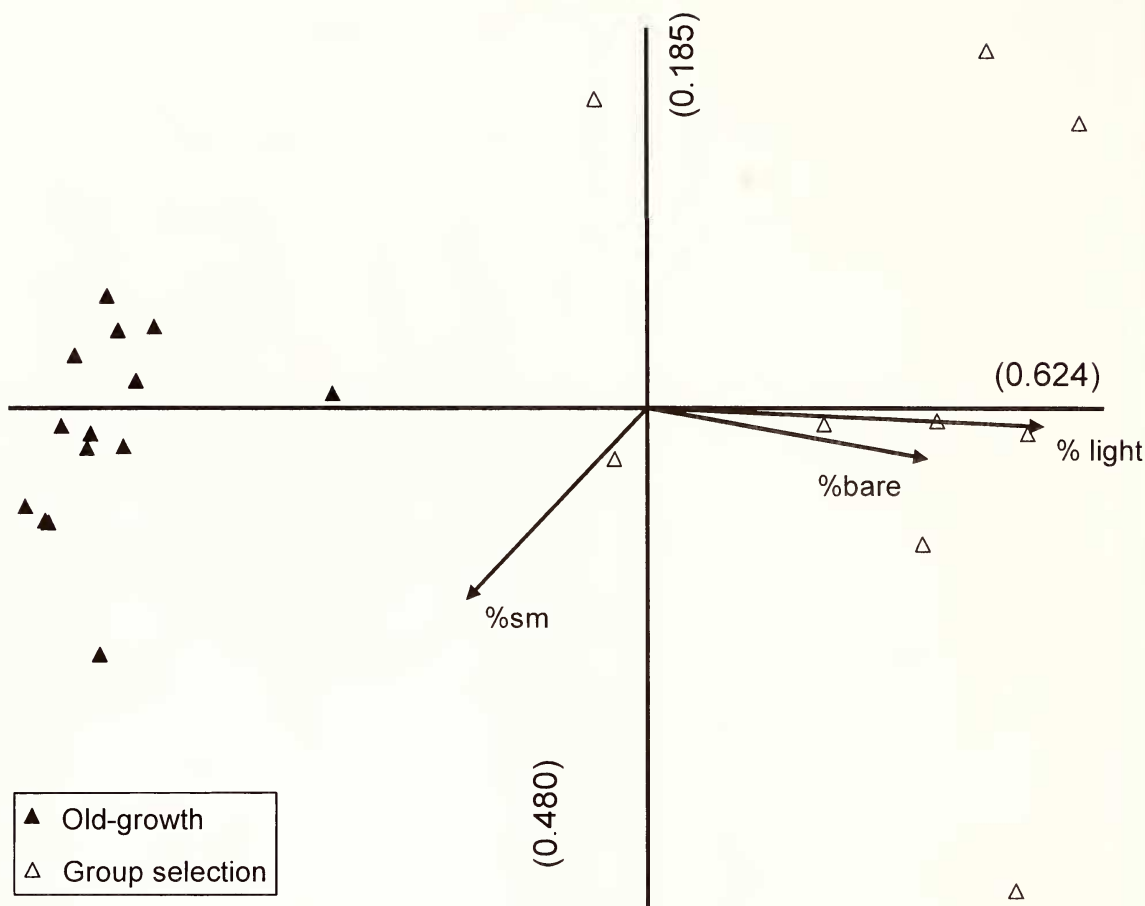
Fig. 2. CCA graph displaying the separation of plots by community according to vegetation and environmental data. Two distinct communities are shown, old-growth and group selection, with no ecotonal edge community in between. The community designation also reflects the TWINSPAN groupings (open vs. closed triangles). CCA eigenvalues are in parenthesis along the axis. The correlation between species and specific environmental parameters are displayed graphically by the rays extending from the origin. The magnitude of the variables effect is depicted by the ray's length and the direction of plot placement by the angle.% sm = soil moisture, % bare = bare soil, %light = % TTR.

lines that radiated from the center along the cardinal directions. All quantitative environmental and botanical sampling was conducted along these lines. For each circular plot, two soil samples were taken at points 5 m north from plot center and 5 m south to a depth of 30 cm. Soil water content (g of water/100 g dry soil) was measured gravimetrically in June 2000. We used hemispherical photographs of the canopy to estimate light availability. Photographs were taken at plot center and points 7 m away from plot center in each cardinal direction at 1 m height. Photographs were analyzed using Gap Light Analyzer software (GLA http://www.rem. sfu.ca/forestry/downloads/gap_light_analyzer.htm) to calculate the percent of total transmitted radiation (%TTR), which estimates long-term average light levels.

We used line-point sampling to measure understory plant abundance and seedbed conditions in each plot. Every 10 cm we noted plant species (no-

menclature follows Hickman 1993) and classified the soil surface as fine litter, course woody debris or bare soil. Plot-level species richness was measured by conducting a timed census (two hr/plot).

We sampled random plots from the interior of the old-growth forest to check for differences with the transect plots at 20 m and 40 m into the old-growth. All interior plots were at least 60 m away from any edge—we refer to these plots as the random old-growth plots. Data collection in these plots followed the procedures described above.

We explored the relationship between the resource gradients and plant composition with canonical correspondence analysis (CCA). We used the CCA to ordinate plots in a state space defined by linear combinations of the environmental variables of light, soil moisture, and seedbed type (Palmer 1993). We used two-way indicator species analysis (TWINSPAN), a divisive clustering program that classifies the plots based on species abundance (van
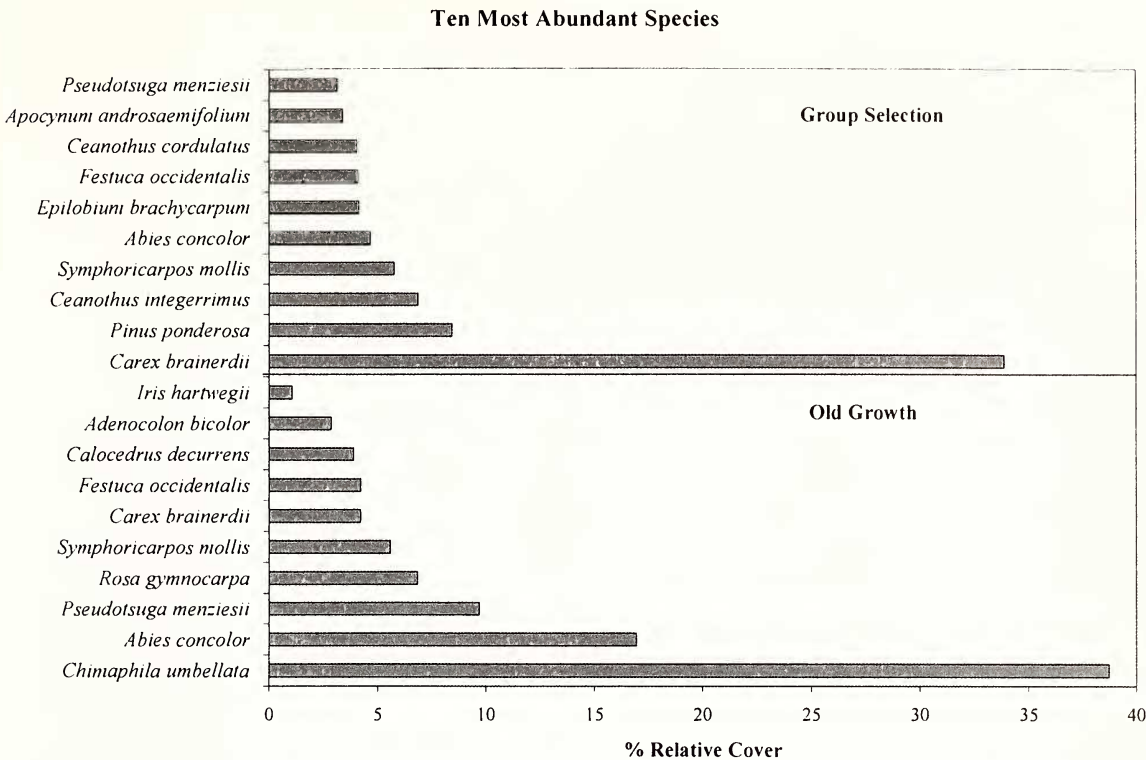
Ten Most Abundant Species

FIG. 3.　Ten most abundant species by percent relative cover in each area: group selection and old-growth.

Tongeren 1995), as an independent measure of plot locations in ordination space. We used PC-ORD version 4 (MJM software, OR) to conduct all ordination and clustering analyses.

We relied on species richness as our primary measure of understory plant diversity. To account for the species-area relationship, we extrapolated species accumulation curves from sequential plot sampling (Colwell and Coddington 1994; Battles et al. 2001). Both species accumulation curves depict richness saturating at approximately nine sampled plots. Thus richness is reported as the mean of nine randomly resampled plots.

RESULTS

We observed a sharp and short gradient between old-growth and group selection plots (Fig. 1). While there was a slight increase in understory light on the edge relative to the nearest old-growth plots (−20), the difference between the edge and the nearest group plots (+20) was large. There were similar sharp increases at the edge in plant abundance as measured by cover and in the fraction of bare soil (Fig. 1).

The multivariate analyses also showed sharp differences between old-growth and group selection plots and did not detect an ecotone community that shares aspects of both communities. The CCA analysis produced two distinct clusters along the pri-

mary ordination gradient (Fig. 2). This primary axis is most correlated with understory light availability. The first division of the TWINSPAN analysis (eigenvalue = 0.480) separated plots into the same groups as the CCA (Fig. 2) with no overlap between old-growth and group selection plots.

These results imply an edge effect on the understory plant community of less than 10 m in either direction. Moreover, we checked for bias in our comparison, in particular whether our plots into the old-growth were representative of the forest, by comparing the old-growth transect plots to the random plots from the interior of the Baker plot. In terms of key environmental metrics (i.e., light availability, seed bed, and soil moisture) and measures of the understory vegetation (i.e., composition, abundance, and species richness), we could detect no differences. At this site, edge effects were confined to a narrow area near the harvest boundary.

The lack of an ecotone is surprising given the differences between the adjacent plant associations. The group selection plots had significantly greater species richness. Based on a minimum sample of nine plots, mean species richness in the old-growth was 55 species (95% CI = 52–57 species). In the group selection, mean richness was 74 species (95% CI = 68–81 species). However, the understory vegetation was dominated by one species in each area (Fig. 3).